

Spurkull constrictor

```

REFERENCE
  #cross-references GB:Ms3294; NID:9339744; PID:AAA03210.1; PID:9339745
  #authors Himmer, A.; Maurer-Fogy, I.; Krenke, M.; Scheurich, P.; Pratzmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.; Stratow, C.; Adolf, G.R.
  #journal DNA Cell Biol. (1990), 9:705-715
  #title Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.

#cross-references MUID:91090841
#accession A3555
#molecule_type mRNA
#residues 1-455 #label HIM
#cross-references GB:Ms3121; NID:9339755; PIDN:AAA36754.1; PID:9339756
#accession C3555
#molecule_type protein
#residues 30-38:41-53,'X',55-79,'XX',82-94,'NK','XX',100-104; 107-128;162-167,'X',169-201 ##label H12
#note the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the receptor

REFERENCE
  #authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
  #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:730-7384
  #title Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A36281
#molecule_type mRNA
#residues 1-155 ##label GRA
#cross-references GB:Ms7764
#note the authors translated the codon TGG for residue 371 as Thr, AGG for residue 372 as Leu, and GAC for residue 427 as Asn

REFERENCE
  #authors Nophar, Y.; Kemper, O.; Brakebusch, C.; Endelmann, H.; Zwang, R.; Adenka, D.; Holtmann, H.; Wallach, D.
  #journal EMBJ (1990) 9:3269-3278
  #title Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.

#cross-references MUID:9106021
#accession S12057

REFERENCE
  #authors RENCE, J.; Kempf, O.; Wallach, D.
  #journal Gene (1993) 134:205-215
  #title Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor (TNF) receptor.
#cross-references MUID:94085779
#molecule_type DNA
#residues 1-13 ##label KEM
#note sequencing

REFERENCE
  #authors JTH758
  #journal Gene (1993) 134:205-215
  #title Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor (TNF) receptor.

#cross-references MUID:94085779
#molecule_type DNA
#residues 1-13 ##label KEM
#note sequencing

REFERENCE
  #authors J.M.
  #journal Eur. J. Immunol. (1990) 20:1167-1174
  #title Tumor necrosis factor inhibitor: Purification, NH2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.

#cross-references MUID:90202116
#accession A60231
#molecule_type protein
#residues 41-43,'X',45-53,'X',55-57 ##label SEC
#length 455 #molecular-weight 50494 #checksum 153

SUMMARY
  Gatnaga, T.; Hwang, C.; Kohn, W.; Cappuccini, F.; Lucci II, J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto, R.S.; Granger, G.A.
  #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
  #title Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.

#cross-references MUID:91062364
#accession A38258
#molecule_type protein
#residues 41-60 ##label GAT
#experimental-source cancer patient serum
#cross-references MUID:89171156
#accession A60594
#molecule_type protein
#residues 41-33,'X',45-53,'V',55-57,'NK',60 ##label OLS
#experimental-source renal failure patient urine
REFERENCE
  #authors Engelman, H.; Novack, D.; Wallach, D.
  #journal Eur. J. Haematol. (1989) 42:270-275
  #title Isolation and characterization of a tumor necrosis factor binding protein from urine.

#cross-references MUID:910110215
#accession A35010
#molecule_type protein
#residues 41-45 ##label ENG
#experimental-source normal urine
REFERENCE
  #authors Kajimura, J.; Asada, A.; Kirihara, S.; Kato, K.
  #journal Biosci. Biotechnol. Biochem. (1994) 58:2265-2268
  #title Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.

#cross-references MUID:910110215
#accession JC2404
#molecule_type protein
#residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 ##label KAJ
#experimental-source urine
#cross-references GDB:125913; OMIM:191190
#gene TNFRSF1A
#map_position 12p13.2-12p13.2
#intons 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
#classification superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
#keywords duplication; glycoprotein; receptor; transmembrane protein
FEATURE
  #cross-references GDB:125913; OMIM:191190
  #product tumor necrosis factor receptor type I ##status Predicted ##label MAT
  #domain extracellular ##status Predicted ##label EXT
  #domain signal sequence ##status Predicted ##label SIG
  #product tumor necrosis factor receptor type I ##status Predicted ##label MAT
  #domain extracellular ##status Predicted ##label EXT
  #product TNF binding protein 1 (tumor necrosis factor alpha inhibitor) ##status Experimental ##label TPB1
  #domain NGF receptor repeat homology ##label NG1
  #domain NGF receptor repeat homology ##label NG2
  #domain NGF receptor repeat homology ##label NG3
  #domain NGF receptor repeat homology ##label NG4
  #domain transmembrane ##status Predicted ##label MEM
  #domain intracellular ##status Predicted ##label INT
  #binding site carbohydrate ##status Predicted ##label ASN
  #predicted Predicted

```

Best Available Copy

Best Available Copy

Shared Comparator A

Query Match 100.0%; Score 202; DB 1; Length 455;
 Best Local Similarity 96.4%; Pred. No. 6. 35e-36; O; Mismatches 1; Indels 0; Gaps 0;
 Matches 27; Conservative 0; Organism

Db 30 LPVHLDREKRDSCPGKVHVKNSI 57
 Qy 1 lvphlgdrekrdscpgkvihpqxnsi 28

RESULT 2
 ENTRY 157826 #type complete
 TITLE tumor necrosis factor receptor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
 ACCESSIONS I57826
 REFERENCE #authors Rothe, J.G.; Bluthmann, H.; Gantz, R.; Lesslauer, W.; Steinmetz, M. (1993) 30:165-176
 #title Mol. Immunol. (1993) 30:165-176
 #cross-references MUID:93156721
 #accession I57826
 #status preliminary; translated from GB/EMBL/DDBJ
 #molecule_type DNA
 #residues 1-454 #label RES
 #cross-references GB:W76656; NID:9202100; PIDN:AAA40465.1; PID:9202102

GENETICS #gene TNFR-2
 #introns 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 25/3; 353/1
 #classification superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
 #keywords FEATURE cytokine receptor
 SUMMARY #domain NGF receptor repeat homology #label NGF
 #length 454 #molecular_weight 50030 #checksum 4267

Query Match 83.7%; Score 169; DB 2; Length 454;
 Best Local Similarity 78.6%; Pred. No. 1.19e-26; O; Mismatches 22; Conservative 3; Indels 0; Gaps 0;
 Matches 3; Mismatches 3; Organism

Db 30 LPVSLGDRERKRDSCPGKVHVKNSI 57
 Qy 1 lvphlgdrekrdscpgkvihpqxnsi 28

RESULT 3
 ENTRY 157827 #type complete
 TITLE tumor necrosis factor receptor 1 precursor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
 ACCESSIONS A38634; Ba0254; S16677; S19021; I54532
 REFERENCE #authors Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.; Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
 #journal Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.
 #cross-references MUID:91187885
 #accession A38634
 #molecule_type mRNA
 #residues 1-454 #label LEW
 #cross-references GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826
 REFERENCE #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A. Mol. Cell. Biol. (1991) 11:3020-3026
 #title Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.

RESULT 4
 ENTRY 157827 #type complete
 TITLE tumor necrosis factor receptor 1 precursor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
 DATE 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change

SUMMARY #length 454 #molecular_weight 50129 #checksum 4839
 Query Match 83.7%; Score 169; DB 1; Length 454;
 Best Local Similarity 78.6%; Pred. No. 1.19e-26; O; Mismatches 22; Conservative 3; Indels 0; Gaps 0;
 Matches 3; Mismatches 3; Organism

Db 30 LPVSLGDRERKRDSCPGKVHVKNSI 57
 Qy 1 lvphlgdrekrdscpgkvihpqxnsi 28

#cross-references MUID:91246168
 #accession B40254
 #molecule_type mRNA
 #residues 1-454 #label GO2
 #cross-references GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826
 REFERENCE #authors Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonergis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J. Eur. J. Immunol. (1991) 21:1649-1656
 #journal Cloning, expression and cross-linking analysis of the murine P55 tumor necrosis factor receptor. #accession S16677
 #molecule_type mRNA
 #residues 1-454 #label BAR
 #cross-references EMBL:X59238; NID:953578; PIDN:CAA41922.1; PID:953579
 REFERENCE #authors Rothe, J.G.; Brockhaus, M.; Gantz, R.; Lesslauer, W.; Immunochemistry (1991) 34:338-340
 #journal Molecular cloning and expression of the mouse TNF receptor
 #title #cross-references MUID:91285014
 #accession S16677
 #molecule_type mRNA
 #residues 1-454 #label ROT
 #cross-references EMBL:X57796; NID:954848; PIDN:CAA40936.1; PID:954849
 REFERENCE #authors Bebo, B.F. Immunogenetics (1994) 39:450-451
 #journal Nucleotide sequence of the TNF type I receptor from a mouse
 #title endothelioma cell line.
 #cross-references MUID:94245292
 #accession I54532
 #molecule_type mRNA
 #residues 1-454 #label RES
 #cross-references GB:L20349; NID:9430732; PIDN:AAA59361.1; PID:9430733
 COMMENT This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
 #classification #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
 #keywords FEATURE duplication; glycoprotein; receptor; transmembrane protein
 #length 454 #molecular_weight 50129 #checksum 4839
 #product tumor necrosis factor receptor type 1 #status predicted #label SIG
 #predicted #label MAT
 #domain extracellular #status predicted #label EXTR
 #domain NGF receptor repeat homology #label NG1
 #domain NGF receptor repeat homology #label NG2
 #domain NGF receptor repeat homology #label NG3
 #domain NGF receptor repeat homology #label NG4
 #domain transmembrane #status predicted #label MEM
 #domain intracellular #status predicted #label INT
 #binding_site carbohydrate (Ash) (covalent) #status predicted
 #predicted
 SUMMARY #length 454 #molecular_weight 50129 #checksum 4839
 Query Match 83.7%; Score 169; DB 1; Length 454;
 Best Local Similarity 78.6%; Pred. No. 1.19e-26; O; Mismatches 22; Conservative 3; Indels 0; Gaps 0;
 Matches 3; Mismatches 3; Organism

Speaker continues to

Selected Comparisons

Query Match Best Local Similarity 96.4%; pred. No. 6.35e-36; Mismatches 0; Indels 0; Gaps 0; matches 27; Conservative 0;

Db 30 LVPFLGDRERKRDSCPQGYVHKNNSI 57
Qy 1 lvpflgdrerkrdsycopqgyvhknnsi 28

RESULT 2
ENTRY 157826 #type complete tumor necrosis factor receptor - mouse
TITLE formal_name Mus musculus #common_name house mouse
ORGANISM 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
DATE 23-Jul-1999

ACCESSIONS
REFERENCE
authors #Journal Rothe, J.G.; Bluthmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M. (1993) 30:165-176
title Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.

#cross-references MUID:33156721
accession 157826
#status preliminary; translated from GB/EMBL/DDJB
#residues 1-454 #label RES
#cross-references GB:M76656; PIDN:AAA404651; PID:9202102

GENETICS
CLASSIFICATION
FEATURE 44-82
KEYWORDS
SUMMARY
Query Match Best Local Similarity 78.6%; Pred. No. 1.19e-26; Mismatches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 30 LVPFLGDRERKRDSCPQGYVHKNNSI 57
Qy 1 lvpflgdrerkrdsycopqgyvhknnsi 28

RESULT 3
ENTRY 154532 #type complete tumor necrosis factor receptor 1 precursor - mouse
ALTERNATE_NAMES tumor necrosis factor receptor, 55k
ORGANISM 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
DATE 22-Jun-1999

ACCESSIONS
REFERENCE
authors Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.; Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
#Journal Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.

#cross-references MUID:9118/885
#cross-references A38634
#cross-references #1-454 #label LEW
#residues
#cross-references GB:M60468; PIDN:AAA397511; PID:9199826

REFERENCE
authors Goodlin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.; Mol. Cell. Biol. (1991) 11:3020-3036
#Journal Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.

RESULT 4
ENTRY 154532 #type complete GQRTW1 tumor necrosis factor receptor 1 precursor - rat
TITLE tumor necrosis factor binding protein 1 (TNF blocking factor)
CONTAINS
ORGANISM 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
DATE 22-Jun-1999

#cross-references MUID:91246168
#accession B40254
#molecule_type mRNA
#residues 1-454 #label GO2
#cross-references GB:M60468; PIDN:9199825; PIDN:AAA397511; PID:9199826
REFERENCE S16677
authors Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissnerorghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
journal Eur. J. Immunol. (1991) 21:1641-1656
#title Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.
#cross-references MUID:911885014
#accession S16677
#molecule_type mRNA
#residues 1-454 #label BAR
#cross-references EMBL:X59238; PIDN:953578; PIDN:CAA419221; PID:953579
REFERENCE S19021
authors Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.; Immunogenetics (1991) 34:338-340
title Molecular cloning and expression of the mouse Tnf receptor type b.
#cross-references MUID:92039815
#accession S19021
#molecule_type mRNA
#residues 1-454 #label RPT
#cross-references EMBL:X57796; PIDN:954848; PIDN:CAA409361; PID:954849
REFERENCE I54532
authors Babo, B.F.
journal Immunogenetics (1994) 39:450-451
#molecule_type mRNA
#residues 1-454 #label RES
#cross-references MUID:94245292
#accession 154532
#status translated from GB/EMBL/DDJB
#molecule_type mRNA
#residues 1-454 #label RPT
COMMENT This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
KEYWORDS duplication; glycoprotein; receptor; transmembrane protein
FEATURE 1-29
Db 30 LVPFLGDRERKRDSCPQGYVHKNNSI 57
Qy 1 lvpflgdrerkrdsycopqgyvhknnsi 28

RESULT 3
ENTRY 30-212 #type complete domain signal sequence #status Predicted #label SIG#status Predicted #label MAT#status Predicted #label EXTN
ALTERNATE_NAMES domain extracellular #status Predicted #label EXTN
ORGANISM 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
DATE 22-Jun-1999

ACCESSIONS
REFERENCE
authors A38634; B40254; S16677; S19021; I54532
#cross-references A38634
#cross-references Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.; Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
#Journal Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.

#cross-references MUID:9118/885
#cross-references A38634
#cross-references #1-454 #label LEW
#residues
#cross-references GB:M60468; PIDN:AAA397511; PID:9199826

REFERENCE
authors A40254
#cross-references Goodlin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.; Mol. Cell. Biol. (1991) 11:3020-3036
#Journal Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.

ACCESSIONS B36555
REFERENCE A36555
#authors Pfleiderer, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
Straatova, C.; Adoli, G.R.
DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.

#cross-references MUID:91090841
#accession B36555
#molecule_type mRNA
#residues 1-461 #label HIM
#cross-references GB:M6122; NID:9207361; PIDN:AAA42256.1; PID:9207362
COMMENT This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
KEYWORDS duplication; glycoprotein; receptor; transmembrane protein
FEATURE F1
1-29
30-461
30-211
30-501
44-82
84-126
127-167
168-204
212-234
235-461
54-151,201
#length 461 #molecular_weight 50969
#predicted
#product tumor necrosis factor receptor type 1 #status predicted #label MAT
#domain extracellular #status Predicted #label EXT
#product tumor necrosis factor binding protein #status predicted #label TBP
#predicted
#domain NCF receptor repeat homology #label NG1
#domain NGF receptor repeat homology #label NG2
#domain NCF receptor repeat homology #label NG3
#domain NCF receptor repeat homology #label NG4
#domain transmembrane #status Predicted #label MEM
#domain intracellular #status Predicted #label INT
#binding_site carbohydrate (Asn) (covalent) #status
#predicted
#length 461 #molecular_weight 50969
#checksum 1617
#summary

Query Match 82.7% Score 167; DB 1; Length 461;
Best Local Similarity 78.6%; Pred. No. 4.2e-26;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 30 LYLHPSDREKRSCPGKYSHQNRSI 57
Qy 1 lvphlgdrekrdsvcpqkylhpqnsi 28

RESULT	6
ENTRY C69980	#type complete
TITLE hypothetical protein Yrr - <i>Bacillus subtilis</i>	
ORGANISM #formal_name <i>Bacillus subtilis</i>	
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998	
ACCESSIONS C69980	
REFERENCE A69580	
#authors	
Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boris, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Conneron, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Ehlich, S.D.; Emmerson, P.T.; Entian, K.D.; Erington, J.; Fabret, C.; Ferrari, E.; Foulier, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fumia, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hojsappel, S.; Hosono, S.; Hullio, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaes-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Konigstein, G.; Krohn, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott, A.M.; Prescan, E.; Puig, P.; Purnelle, B.; Rapoport, G.; Rev, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scuffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Seror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Taccioni, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Totsuka, V.; Uchiyama, S.; Vandenberg, M.; Vanner, F.; Vassarotti, A.; Viati, S.; Wambutt, R.; Wedler, E.; Wedler, H.; Weitzneger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Kata, K.; Yoshida, K.; Yoshioka, H.F.; Zunstein, E.; Yoshioka, H.; Danchin, A.	
RESULT 5	
ENTRY JC4302	#type complete
TITLE tumor necrosis factor receptor p55 precursor - pig	
ORGANISM #common_name <i>Sus scrofa domestica</i> #common_name domestic pig	
DATE 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999	
ACCESSIONS JC4302	
REFERENCE JC4303	
#authors Suter, B.; Pauli, U.	
Gene (1995) 163:263-266	
#title Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.	
#cross-references MUID:9601625	
#accession JC4302	
#molecule_type mRNA	
#residues 1-461 #label SUT	
#cross-references GB:U19944; NID:91141752; PIDN:AAC48499.1; PID:91141753	
#accession PC4093	
#molecule_type Protein	
#residues 1-7 #label SU2	
GENETICS #experimental_source kidney cell line 15	
CLASSIFICATION tnf superfAMILY tumor necrosis factor receptor type 1; NGF receptor repeat homology	
KEYWORDS glycoprotein; kidney; receptor; transmembrane protein; tumor	
FEATURE #gene tnf	
#cross-references MUID:98044033	
#accession C69980	
#status preliminary; nucleic acid sequence not shown; translation not shown	

1-29
30-461
44-194
44-82
84-126
211-231
361-447
#domain signal sequence #status predicted #label SIG
#product tumor necrosis factor receptor p55 #status predicted
#predicted #label MAT
#domain extracellular cysteine rich #status predicted
#label EXT
#domain NGF receptor repeat homology #label NG1
#domain NCF receptor repeat homology #label NG2
#domain transmembrane #status predicted #label TMR
#domain signal transduction #status predicted #label SRM
#binding_site carbohydrate (Asn) (covalent) #status predicted
#predicted

SUMMARY Query Match 76.7%; Score 155; DB 2; Length 461;
Best Local Similarity 75.0%; Pred. No. 8.18e-23;
Matches 21; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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##molecule_type DNA
##residues 1-213 ##label KUN
##cross-references GB:299117; PID:AL009126; NID:92634966; PID:e1183958;
##experimental_source strain 168

#TICS
#ARY
#gene
#length 213 #molecular-weight 24196 #checksum 2669
#YRT
#length 213 #molecular-weight 55571 #checksum 5540
#FAD; oxidoreductase
#KEYWORDS
#length 506 #molecular-weight 55571 #checksum 5540
#SUMMARY
#Query Match 31.2%; Score 63; DB 2; Length 506;
#Best Local Similarity 30.0%; Pred. No. 1.57e+00; Mismatches 5; Indels 0; Gaps 0;
#Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

#LT
# 7
#H70388 #type complete
#selenophosphate synthase - Aquifex aeolicus
#formal_name Aquifex aeolicus
#8-May-1998 #sequence_revision 08-May-1998 #text_change
#R70388
#A70300
#Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Sneed, M.A.; Keller, M.; Auyu, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.
#Nature (1998) 392:353-358
#The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
#cross-references MUND:98196666
#accession H70388
#status preliminary; nucleic acid sequence not shown;
#translation not shown
##molecule_type DNA
##residues 1-311 ##label AQF
##cross-references EMBL:AB001719; NID:g2983517; PID:g2983519; GB:AE000657
##experimental_source strain VF5

#LT
# 8
#H70388
#type complete
#probable squalene monooxygenase (EC 1.14.99.7) Sqp1 - rape
#formal_name Brassica napus #common_name rape
#E
#N
#S
#C
#G
#P
#JOURNAL
#title
#journal
#organism
#accession
#status
#translated from GB/EMBL/DDJB
##molecule_type mRNA
##residues 1-518 ##label SCH
##cross-references EMBL:AJ05928; NID:e1291748; PID:e1291749
##experimental_source cv. Westar; developmental stage: thaliana and Brassica napus.
#T07940
#GENETICS
#ARY
#length 311 #molecular-weight 34231 #checksum 842
#RESULT
#9
#T07940 #type complete
#probable squalene monooxygenase (EC 1.14.99.7) Sqp2 - rape
#formal_name Brassica napus #common_name rape
#KEYWORDS
#SUMMARY
#Query Match 31.2%; Score 63; DB 2; Length 518;
#Best Local Similarity 30.0%; Pred. No. 1.57e+00; Mismatches 5; Indels 0; Gaps 0;
#Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
#Db
#75 HYTERDMRPRVYRMGEFMP 94
#QY
#4 hlgarekrdsvcpqkyihp 23

#LT
# 8
#T07942 #type complete
#probable squalene monooxygenase (EC 1.14.99.7) Sqp1 - rape
#formal_name Brassica napus #common_name rape
#E
#N
#S
#C
#G
#P
#JOURNAL
#title
#journal
#organism
#accession
#status
#translated from GB/EMBL/DDJB
##molecule_type DNA
##residues 1-518 ##label GAR
##cross-references EMBL:212617; NID:g60497; PID:CA78263.1; PID:g60498
##molecule_type mRNA
#T07942
#An example of intron junctional sliding in the gene families encoding squalene monooxygenase homologues in Arabidopsis thaliana and Brassica napus.
#CLASSIFICATION
#superfamily influenza virus hemagglutinin
#summary #length 563 #molecular-weight 6283 #checksum 792

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 Best Local Similarity 33.3%; Pred. No. 1.57e+00; Indels 0; Gaps 0;
 Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 97 ERRERNNDVCYFGKFVNGE 114
 Qy 7 dikrkdsvcpqkylnpq 24

RESULT 11 S57335 #type complete cleavage and polyadenylation specificity factor 160K chain - bovine.
 formal_name Bos primigenius taurus #common_name cattle
 28-oct-1995 #sequence_revision 03-Nov-1995 #text_change
 10-Sep-1997
 ACCESSIONS S57335; S57333
 REFERENCE #authors Jenny, A.; Keller, W.
 Nucleic Acids Res. (1995) 23:2629-2635
 #title Cloning of cDNAs encoding the 160 kDa subunit of the bovine cleavage and polyadenylation specificity factor.
 #cross-references MUID:95380277
 #accession S57335
 #status nucleic acid sequence not shown
 #molecule_type mRNA
 #residues 1-144 #label JEN
 #cross-references EMBL:X83097; NID:953171; PID:9929007
 #accession S57333
 #molecule_type protein
 188-197-204-216; 403-423-426-437; 511-519; 572-580; 780-789;
 1107-1116; 1163-1167; 1280-1289; 1301-1314; 1422-1444
 #length 1444 #molecular_weight 161213 #checksum 3312
 SUMMARY
 Query Match 31.2%; Score 63; DB 2; Length 1444;
 Best Local Similarity 28.6%; Pred. No. 1.57e+00; Indels 1; Gaps 1;
 Matches 8; Conservative 11; Mismatches 8; Indels 1; Gaps 1;
 Db 1048 VPRMTGEEKEFETTIERDERYHPPQAF 1075
 Qy 2 vphlgdekr-dsvcpqkylnpqnsi 28

RESULT 12 S47023 #type complete DNA-directed RNA polymerase (EC 2.7.7.6) chain D - Sulfolobus acidocaldarius
 #formal_name Sulfolobus acidocaldarius
 #text_change 13-Jan-1995 #sequence_revision 13-Jan-1995
 DATE 18-Jun-1999
 ACCESSIONS S47223
 REFERENCE #authors Lamer, D.; Hain, J.; Thuriiaux, P.; Zillig, W.
 #submission submitted to the EMBL Data Library, July 1994
 #description similarity of the transcription systems of Eucharya and Archaea.
 #accession S47023
 #molecule_type DNA
 #residues 1-264 #label LAN
 #cross-references EMBL:X80194; NID:9517286; PID:NCA56480.1;
 GENETICS
 #gene rpoD
 CLASSIFICATION #superfamily DNA-directed RNA polymerase II chain RPB3;
 #domain ferrredoxin 2[4Fe-4S] homology
 KEYWORDS nucleotidyltransferase; transcription
 FEATURE FER
 163-220
 SUMMARY #length 264 #molecular_weight 29812 #checksum 8558
 Qy Match 30.7%; Score 62; DB 2; Length 264;

RESULT 13 B72775 #type complete probable DNA replication licensing factor ncm APE0188 - aeropyrum pernix (strain K1)
 formal_name Aeropyrum pernix
 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
 DATE B72775
 ACCESSIONS A77450
 REFERENCE #authors Kawabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikara, Y.; Jin-no, K.; Takahashi, M.; Sekine, M.; Baba, S.; Anai, A.; Kosugi, H.; Hosoyama, A.; Fukui, S.; Nagai, Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, I.; Kudo, I.; Imanzaki, J.; Kishida, N.; Oguchi, A.; Aoki, K.; Kubota, K.; Nakamura, Y.; Nomura, N.; Sako, Y.; Kikuchi, H.
 DNA Res. (1999) 6:83-101
 #title Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix K1.
 #cross-references MUID:99310339
 #accession B72775
 #status preliminary
 #molecule_type DNA
 #residues 1-659 #label RAW
 #cross-references DDBJ:AP00058; NID:95103388; PIDN:DAA79100.1;
 #experimental_source strain K1
 GENETICS
 #gene APE0188
 SUMMARY #length 699 #molecular_weight 78685 #checksum 2411
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 Best Local Similarity 58.3%; Pred. No. 2.43e+00; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 166 LGERIEPSPICP 177
 Qy 5 lgdrekdsvp 16

RESULT 14 E71330 #type complete probable preprotein translocase subunit (secA) - syphilis spirochete
 #formal_name Treponema pallidum subsp. pallidum #common_name syphilis spirochete
 #text_change 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
 DATE 20-Aug-1999
 ACCESSIONS E71330
 REFERENCE #authors Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwynn, M.; Hickley, E.K.; Clayton, R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Peterson, J.; Kholak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald, L.; Artlach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.; Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Watthey, L.; Weidman, J.; Smith, H.O.; Ventur, J.C.
 Science (1998) 281:375-388
 #journal Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 #cross-references MUID:9833770
 #accession E71330
 #status preliminary; nucleic acid sequence not shown;
 translation not shown;

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##molecule_type DNA
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##cross-references GB:AE001217; GB:AP000520; NID:g3322655;
##experimental_source strain Nichols
##genetic PID:AA65365.1; PID:g3322659
GENETICS
CLASSIFICATION TP0379
#superfamily preprotein translocase seCA; DEAD/H box helicase
FEATURE homology
KEYWORDS ATP; P-loop
SUMMARY
103-599 #domain DEAD/H box helicase homology #label DEAD\A
103-110 #region nucleotide-binding motif A (P-loop)\B
210-213 #region nucleotide-binding motif B\A
#length 916 #molecular-weight 103779 #checksum 4056

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Query Match Similarity 30.7%; Score 62; DB 2; Length 916; Best Local Similarity 25.9%; Pred. No. 2.43e+00; Matches 7; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Db 433 WYVLSSEKWSATCDEIKEANTHQQPV 459
Qy 2 vphlgdrekrdsvcpqgyihpqxsi 28

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RESULT 15
ENTRY S63986 #type fragment
TITLE collagen alpha 5 chain - sea urchin (Strongylocentrotus
ORGANISM purpuratus) (fragment)
DATE 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change
ACCESSIONS 25-Apr-1997
REFERENCE S63986; S64638
#authors Expósito, J.Y.; Boute, N.; Deleage, G.; Garrone, R.
#journal Eur. J. Biochem. (1995) 234:59-65
#title Characterization of two genes coding for a similar
four-cysteine motif of the amino-terminal propeptide of a
sea urchin fibrillar collagen.
#cross-references MURID:96096722
#accession S63986
#status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-1376 ##label EXP
##cross-references EMBL:X89804
REFERENCE S64637
#authors Expósito, J.Y.
#submission submitted to the EMBL Data Library, July 1995
#accession S64638
##molecule_type DNA
##residues 1-658, 'G', 660-870, 'G', 872-901, 'H' 903-1185, 'T',
1187-1214, 'Y', 1216-1376 ##label EXP
#cross-references EMBL:X89804
GENETICS
#gene COLPsa1alpha
#introns 73/1; 136/2; 221/1; 369/1; 517/1; 659/1; 799/1; 948/1;
1033/1; 1236/1
CLASSIFICATION #superfamily von Willebrand factor type C repeat homology
FEATURE extracellular Matrix
#domain von Willebrand factor type C repeat homology
15-73 #label VWC
SUMMARY
#length 1376 #checksum 7553

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Search completed: Tue Apr 18 11:06:48 2000
Job time : 53 secs.

RL DNA Cell Biol. 9:705-715(1990).
 RN [5]
 RP
 SSQUENCE FROM N.A.
 TISSUE-PLACENTA;
 MEDLINE; 91017509.
 RA GRAY P.W.; BARRETT K.; CHAWRY D.; TURNER M.; FELDMAN M.;
 RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
 expression of recombinant soluble TNF-binding protein.";
 Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX
 RA MEDLINE: 92250049.
 RA FUCHS P.; SUREHL S.; DWORAK M.; HIMMEL A.; AMBROS P.F.;
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
 localization to chromosome 12p13.";
 Genomics 13:219-224(1992).
 RN [7]
 RP SEQUENCE OF 41-45.
 RX
 RA MEDLINE: 90110215.
 RA ENGELMANN H.; NOVICK D.; WALLACH D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 urine. Evidence for immunological cross-reactivity with cell surface
 tumor necrosis factor receptors";
 RT J. Biol. Chem. 265:1531-1536(1990).
 RN [8]
 X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
 RX
 MEDLINE: 93258809.
 RA BANNER D.W.; D'ARCY A.; JAMES W.; GENTZ R.; SCHOENFELD H.-J.;
 RA BROGER C.; LOETSCHER H.; LISSLAUER W.;
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
 beta complex: implications for TNF receptor activation.";
 Cell 73:431-445(1993).
 RN [9]
 X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
 RX
 MEDLINE: 97094982.
 RA MAISCHNER J.R.; DEWINE T.O.; KHONO H.; SPRANG S.R.;
 RT "Structures of the extracellular domain of the type I tumor necrosis
 factor receptor";
 Structure 4:1251-1262(1996).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 RECruits CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 SUBSEQUENT CASCADE OF CASPASES (ASPARTATE SPECIFIC CYSTEINE
 PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
 NONCYTOKIDAL TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
 OF THE ACID SPINGOMYELINASE.
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 HOMOPAIRMIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 WITH THE DEATH DOMAIN OF TRADD. VARIOUS DEAD-INTERACTING
 PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 NF-KAPPA B SIGNALING.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
 THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
 NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
 CC -1- SIMILARITY: CONTAINS A LIA-NSP/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME=PROW; NAME=CD guide CD120a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/Prok/CD/cd120a.htm".
 CC
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 or send an email to license@isb-sib.ch).
 DR EMBL; X55313; CAA39021.1; -
 DR M33294; AAA03210.1; -
 DR
 a 3

DR EMBL; M58286; AAA36753.1; -
 DR EMBL; M63121; AAA36734.1; -
 DR EMBL; M75866; AAA61201.1; -
 DR EMBL; M75864; AAA6101.1; JOINED.
 DR EMBL; M60275; AAA36736.1; -
 DR EMBL; A21522; CAA01558.1; -
 DR EMBL; A34899; Q9QH11.
 DR PIR; A35010; A35010.
 DR PIR; S12057; S12057.
 DR PIR; A38208; A38208.
 DR PDB; 1TNR; 31-JUL-94.
 DR PDB; 07-DEC-95.
 DR PDB; 1EXT; 11-JAN-97.
 DR MM: 191190; -
 DR PROSITE; PS0052; TNFR_NGR_1; 3.
 DR PROSITE; PS0050; TNFR_NGR_2; 3.
 DR PPFM; PF0020; TNFR_C6; 4.
 DR PPFM; PF0031; death; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
 KW 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 455
 FT CHAIN 41 291
 FT DOMAIN 22 211
 FT TRANSMEM 212 234
 FT DOMAIN 43 455
 FT DOMAIN 43 196
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 338 348
 FT DOMAIN 356 441
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 145 145
 FT CARBOHYD 151 151
 FT CONFLICT 412 412
 FT CONFLICT 443 445
 SQ SEQUENCE 455 AA: M0494 MW: CE0EA06F CRC32:
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 Best Local Similarity 90.4%; Pred. No. 2.05e-41;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db	30	LVPHLGDREKKRDPSVCPOCKYIHPQNNT 57
Qy	1	1vpfhlgdrekrdpsvcpgkyihpqxnsi 28

OC Butcheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] SEQUENCE FROM N.A.
 RP DR EMBL; M59377; AAA40464.1;
 RX DR EMBL; X59238; CAA4922.1; -.
 MEDLINE; 91187885.
 RA DR EMBL; X57796; CAA40336.1; -.
 RA DR EMBL; L26349; AAA59361.1; -.
 RA DR EMBL; M76656; AAA0465.1; -.
 RA DR EMBL; M88067; AAA40465.1; JOINED.
 RT DR EMBL; M76655; AAA40465.1; JOINED.
 RT DR PIR; A38634; GOMSTI.
 RT DR PIR; S16677; S16677.
 RL DR PIR; S19021; S19021.
 RN DR HSSP; P19438; 1EXT.
 RP DR MGDB; MGI:1314884; TNFRSF1A.
 RX DR PROSITE; PS5050; TNFR_NGFR_2; 3.
 RA DR PROSITE; PS5001; DEATH_DOMAIN; 1.
 RT DR PFAM; PF00020; TNFR_c6; 4.
 RL DR PFAM; PF00531; death_1; -.
 Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3] SEQUENCE FROM N.A.
 RP DR Receptor; transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 RX DR SIGNAL 1 21 POTENTIAL.
 MEDLINE; 91283014.
 RA FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.
 RA FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
 BARBETT, K., TAYLOR-FISHWICK, D.A., COPE, A.P., KISSONERGHIS, A.M.,
 GRAY, P.W., FELDMANN, M., FOXWELL, B.M.J.; "Molecular cloning and expression and cross-linking analysis of the murine p55
 "Cloning, expression and cross-linking analysis of the murine p55
 tumor necrosis factor receptor";
 Eur. J. Immunol. 21:1649-1656(1991).
 RN [4] SEQUENCE FROM N.A.
 RP DR TISSUE-SPLEEN;
 RC DR MEDLINE; 9203815.
 RX DR BEBO, B.F., LINHICUM, D.S.;
 ROTH, J.G., BROCKHAUS, M., GENZ, R., LESSLAUER, W.; "Molecular cloning and expression of the mouse Tnf receptor type b.,";
 RLT ImmunoGenetics 34:338-340(1991).
 RN [5] SEQUENCE FROM N.A.
 RP DR MEDLINE; 94242292.
 RX DR BEBO, B.F., LINHICUM, D.S.;
 ROTH, J.G., BROCKHAUS, M., GENZ, R., LESSLAUER, W.; "Nucleotide sequence of the TNF type I receptor from a mouse
 endometrioma cell line.,";
 RLT Immunogenetics 39:450-451(1994).
 RN [6] SEQUENCE FROM N.A.
 RP DR MEDLINE; 93156721.
 RA DR ROTH, J., BLUMHORN, H., GENTZ, R., LESSLAUER, W., STEINMETZ, M.; "Genomic organization and promoter function of the murine tumor
 necrosis factor receptor beta gene.,";
 RLT Immunol. 30:165-175(1993).
 CC DR -1. FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC DR -1. SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 HOMOTIMERIZATION. ONCE AGGREGATED, THE RECEPTORS DEATH DOMAINS
 WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 PROTEINS SUCH AS TRAF, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC DR -1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC DR -1. SIMILARITY: CONTAINS A LA_NGFR/TNF-TYPE CYSTEINE-RICH REGION.

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DR DR EMBL; M59377; AAA40464.1;
 DR DR EMBL; X59238; CAA4922.1; -.
 DR DR EMBL; X57796; CAA40336.1; -.
 DR DR EMBL; L26349; AAA59361.1; -.
 DR DR EMBL; M76656; AAA0465.1; -.
 DR DR EMBL; M88067; AAA40465.1; JOINED.
 DR DR EMBL; M76655; AAA40465.1; JOINED.
 DR DR PIR; A38634; GOMSTI.
 DR DR PIR; S16677; S16677.
 DR DR PIR; S19021; S19021.
 DR DR HSSP; P19438; 1EXT.
 DR DR MGDB; MGI:1314884; TNFRSF1A.
 DR DR PROSITE; PS5050; TNFR_NGFR_2; 3.
 DR DR PROSITE; PS5001; DEATH_DOMAIN; 1.
 DR DR PFAM; PF00020; TNFR_c6; 4.
 DR DR PFAM; PF00531; death_1; -.
 DR DR Receptor; transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 DR DR SIGNAL 1 21 POTENTIAL.
 DR DR CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.
 DR DR DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
 DR DR TRANSEM 213 235 POTENTIAL.
 DR DR DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
 DR DR DOMAIN 43 196 4 X TNFR-CYS.
 DR DR REPEAT 43 82 TNFR-CYS 1.
 DR DR REPEAT 83 125 TNFR-CYS 2.
 DR DR REPEAT 126 166 TNFR-CYS 3.
 DR DR REPEAT 167 196 TNFR-CYS 4.
 DR DR DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).
 DR DR DOMAIN 356 441 DEATH DOMAIN.
 DR DR DISULPID 102 117 BY SIMILARITY.
 DR DR DISULPID 102 117 BY SIMILARITY.
 DR DR DISULPID 105 125 BY SIMILARITY.
 DR DR DISULPID 127 143 BY SIMILARITY.
 DR DR DISULPID 144 158 BY SIMILARITY.
 DR DR DISULPID 146 158 BY SIMILARITY.
 DR DR DISULPID 149 166 BY SIMILARITY.
 DR DR DISULPID 168 168 BY SIMILARITY.
 DR DR DISULPID 168 179 BY SIMILARITY.
 DR DR DISULPID 179 191 BY SIMILARITY.
 DR DR DISULPID 182 195 BY SIMILARITY.
 DR DR DISULPID 185 195 BY SIMILARITY.
 DR DR DISULPID 195 204 BY SIMILARITY.
 DR DR CARBOHYD 154 54 POTENTIAL.
 DR DR CARBOHYD 151 151 POTENTIAL.
 DR DR CARBOHYD 201 202 POTENTIAL.
 DR DR CONFFLICT 202 202 POTENTIAL.
 DR DR CONFFLICT 394 394 R -> G (IN REF. 6).
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 DR DR OY 1 lvphlgdrekrdsvcpqgkyihpqnsi.28
 DR DR Query Match 83.7% Score 169; DB 1; Length 454;
 DR DR Best Local Similarity 78.6%; Pred. No. 8 20e+31; 3; Mismatches 3; Indels 0; Gaps 0;
 DR DR Matches 22; Conservative 3;
 DR DR SEQUENCE 3

RESULT 3 STANDARD; PRT; 461 AA.
 ID TNFR1_RAT
 AC P22934;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR_1 PRECURSOR (P60) (TNF-RL) (P55).
 CC TNFR1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Butcheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1] SEQUENCE FROM N.A.
 RP DR MEDLINE; 9109841.
 RX DR LANTZ, M., OLSSON, I., HAUPPTMANN, R., STRATOWA, C., ADOLF, G.R.;
 RA DR FIZENMAIER, K.,

RT "Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";
 RT DNA Clin. Biol. 9:705-715(1990).
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUTS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED, THE RECEPTORS DEATH DOMAINS WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNF-TYPE CYSTEINE-RICH REGION.

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CC DR EMBL; MG3122; AAA42256.1; -.
 CC DR PDB; B65555.
 CC DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC DR PROSITE; PS0017; DEATH_DOMAIN; 1.
 CC DR PFAM; PF00020; TNFR_C6; 4.
 CC DR PRAM; PF00531; death; 1.
 CC KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 CC FT SIGNAL 1 21 POTENTIAL.
 CC FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR 1.
 CC FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 234 461 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 235 196 4 X TNFR-CYS.
 CC FT REPEAT 43 196 TNFR-CYS 1.
 CC FT REPEAT 83 125 TNFR-CYS 2.
 CC FT REPEAT 126 166 TNFR-CYS 3.
 CC FT REPEAT 167 196 TNFR-CYS 4.
 CC FT DOMAIN 344 354 N-SMASE ACTIVATION DOMAIN (NSD).
 CC FT DOMAIN 363 448 DEATH DOMAIN.
 CC FT DISULFID 44 58 BY SIMILARITY.
 CC FT DISULFID 59 72 BY SIMILARITY.
 CC FT DISULFID 62 81 BY SIMILARITY.
 CC FT DISULFID 84 99 BY SIMILARITY.
 CC FT DISULFID 102 117 BY SIMILARITY.
 CC FT DISULFID 105 125 BY SIMILARITY.
 CC FT DISULFID 127 143 BY SIMILARITY.
 CC FT DISULFID 146 158 BY SIMILARITY.
 CC FT DISULFID 149 166 BY SIMILARITY.
 CC FT DISULFID 168 179 BY SIMILARITY.
 CC FT DISULFID 182 191 BY SIMILARITY.
 CC FT DISULFID 185 195 BY SIMILARITY.
 CC FT CARBOHYD 154 54 POTENTIAL.
 CC FT CARBOHYD 151 151 POTENTIAL.
 CC FT CARBOHYD 201 201 POTENTIAL.
 SQ SEQUENCE 461 AA; 50969 MW; 82F68B08 CRC32;

Query Match Score 82.7%; Best Local Similarity 78.6%; Matches 22; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy	1 lvphlgdrekrdsvcpqkqkyihpqxnsi 28
RESULT	4
ID	TNRL_PIG
NAME	STANDARD;
PRT	461 AA.
AC	P50555;
DT	01-OCT-1996 (Rel. 34, Created)
DR	01-OCT-1996 (Rel. 34, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN	TNFRSF1A OR TNFR1.
OS	Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Buteraria; Cetartiodactyla; Suina; Suidae; Sus.
RN	[1]
RP	SEQUENCE FROM N. A.
RC	TISSUE-KIDNEY;
RX	MEDLINE; 9801145.
RA	SUTER B., PAULI U.H.;
RT	"Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor."
RL	Gene 163: 263-266 (1995).
CC	-!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUTS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC	-!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED, THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-!- SIMILARITY: CONTAINS A LA-NGFR/TNF-TYPE CYSTEINE-RICH REGION.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/)
CC	DR EMBL; 019994; AAC48499.1; -. CC DR HSSP; P19438; TNFR. CC DR PROSITE; PS00652; TNFR_NGFR_1; 3. CC DR PROSITE; PS0050; TNFR_NGFR_2; 2. CC DR PROSITE; PS0017; DEATH_DOMAIN; 1. CC DR PFAM; PF00020; TNFR_C6; 3. CC DR PRAM; PF00531; death; 1. CC KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis. CC FT SIGNAL 1 21 POTENTIAL. CC FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR 1. CC FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL). CC FT TRANSMEM 211 233 POTENTIAL. CC FT DOMAIN 234 461 CYTOPLASMIC (POTENTIAL). CC FT DOMAIN 43 195 4 X TNFR-CYS. CC FT REPEAT 43 82 TNFR-CYS 1. CC FT REPEAT 83 125 TNFR-CYS 2. CC FT REPEAT 126 166 TNFR-CYS 3. CC FT REPEAT 167 195 TNFR-CYS 4. CC FT DOMAIN 340 350 N-SMASE ACTIVATION DOMAIN (NSD). CC FT DOMAIN 362 447 DEATH DOMAIN. CC FT DISULFID 44 58 BY SIMILARITY. CC FT DISULFID 59 72 BY SIMILARITY. CC FT DISULFID 62 81 BY SIMILARITY. CC FT DISULFID 84 99 BY SIMILARITY. CC FT DISULFID 105 125 BY SIMILARITY.

Query Match 76.7%; Score 155; DB 1; Length 461;
 Best Local Similarity 75.0%; Pred. No. 1.9e-26; PRT; 336 AA.
 Matches 21; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 30 LVIHPGSDREKRESLCPGKYSHRNQNSI 57
 Qy 1 lvphlgarekrdsvcpqkyihpqxnsi 28

RESULT 5
 ID SEDL_AQUAE STANDARD; PRT; 336 AA.
 AC 067139;
 DT 15-DEC-1999 (Rel. 39, Created)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE SELENIDE, WATER DINKINASE (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE)
 DE (SELENUM DONOR PROTEIN).
 DE SELD OR AQ_1030.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 [1] SEQUENCE FROM N.A.

RX STRAIN=VF5;
 RC MEDLINE: 9819666.
 RA DECKER G., WARREN P.V., GASTERLAND T., YOUNG W.G., LENOX A.L.,
 GRAHAM D.E., OVERBEEK R., SNEAD M., AUDAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.",
 RL Nature 392:353-358(1998).
 [2] FUNCTION: CONCEPTUAL TRANSLATION.

RA BAIRACH A.;
 RL Unpublished observations (JUL-1999).

CC (BY SIMILARITY)

- 1- CATALYTIC ACTIVITY: ATP + SELENIDE + H(2)O = AMP + SELENOPHOSPHATE + PHOSPHATE.
- 1- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).
- 1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A UGA STOP CODON HAD TO BE SKIPPED IN POSITION 13 TO PRODUCE THIS ORF. WE (REF.2.) BELIEVE THAT THIS RESIDUE IS MOST PROBABLY AN ACTIVE-SITE SELENOCYSTEINE.
- 1- SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.

CC CLASS I SUBFAMILY.

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DR EMBL; AB000719; AAC07095.1; ALT FRAME.

DR PRM; PR0056; ARRS; 1; KW Transferase; Selenide; Magnesium; ATP-binding; Selenocysteine.

FT ACT_SITE 13 13 POTENTIAL.

FT SITE 13 13 IMPORTANT FOR CATALYTIC ACTIVITY (BY SIMILARITY).

FT NP_BIND 222 228 ATP (POTENTIAL).

RESULT 6
 ID CPSA_HUMAN STANDARD; PRT; 1442 AA.
 AC 010570;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CPSP)
 DE 160 KD SUBUNIT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Butharia; Primates; Catarrhini; Hominidae; Homo.
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE: 96067159.
 RA MURPHY K.G.; MANLEY J.I.;
 RA "The 160-kD subunit of human cleavage-polyadenylation specificity factor coordinates pre-mRNA 3'-end formation.",
 RT Genes Dev. 9:2672-2683(1995),
 CC -1- FUNCTION: CPSF PLAYS A KEY ROLE IN PRE-mRNA 3' END FORMATION,
 CC RECOGNIZING THE AUAAA SIGNAL SEQUENCE AND INTERACTING WITH
 CC POLY(A) POLYMERASE AND OTHER FACTORS TO BRING ABOUT CLEAVAGE AND
 CC STEP OF THE POLYADENYLATION REACTION.
 CC -1- SUBUNIT: CPSF IS A HETEROOTETRAMER COMPOSED OF FOUR DISTINCT
 CC SUBUNITS 150, 100, 70 AND 30 KD.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.

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DR EMBL; US7012; AAC0293.1; KW Nuclear protein; RNA-binding. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 893 908 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

SQ SEQUENCE 1442 AA; 160822 MW; 829675B CRC32;

Query Match 31.2%; Score 63; DB 1; Length 1442;
 Best Local Similarity 28.8%; Pred. No. 3.9e-01; 8; Mismatches 8; Indels 1; Gaps 1;

Db 1047 IPMTGEKEFEITERDIRRYHQEQAF 1074
 Qy 2 vphlgarekrdsvcpqkyihpqxnsi 28

RESULT 7
 ID CPSA_BOVIN STANDARD; PRT; 1444 AA.
 AC 010569;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CPSP)
 DE 160 KD SUBUNIT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.

RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP
 RC TISSUE=THYMUS;
 RX MEDLINE; 95380277;
 RA JENNY A., KELLER W.;
 RT Cloning of cDNAs encoding the 160 kDa subunit of the bovine cleavage
 and polyadenylation specificity factor ";

Nucleic Acids Res, 23:2629-2635(1995).

RN [2] CHARACTERIZATION.

RP
 MEDLINE: 9209544.

RA KELLER W., BIENROTH S., LANG K.M., CHRISTOFORI G.; specifically interacts with
 *Cleavage and polyadenylation factor CCF with
 the pre-mRNA 3'-processing signal AAUAAA.;"

RL EMBO J. 10:4241-4249(1991).

CC FUNCTION: CPSF PLAYS A KEY ROLE IN PRE-MRNA 3'-END FORMATION,
 RECOGNIZING THE AAUAAA SIGNAL SEQUENCE AND INTERACTING WITH
 POL(A) POLYMERASE AND OTHER FACTORS TO BRING ABOUT CLEAVAGE AND
 POL(Y) ADDITION. THIS SUBUNIT IS INVOLVED IN THE RNA RECOGNITION
 STEP OF THE POLYADENYLATION REACTION.

-I- SUBUNIT: CPSF IS A HETERTETRAMER COMPOSED OF FOUR DISTINCT
 SUBUNITS 160, 100, 70 AND 30 KD.

-I- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.

-I- PTM: THE N-TERMINUS IS BLOCKED.

CC -----

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 or send an email to license@isb-sib.ch).

CC -----

CC DR EMBL; X80194; CAA55480.1; --.

DR PIR; S47023; S47023.

DR PROSITE; PS00446; RNA_POL-D_30KD; 1.

DR RNA-directed RNA Polymerase; Transcription,
 Transferase; DNA-directed RNA Polymerase; Transcription,
 Sequence 264 AA; 29812 MW; C55B491B CRC32;

DR -----

DR Query Match 30.7%; Score 62; DB 1; Length 264;
 Best Local Similarity 47.4%; Pred. No. 6.40e-01; O;

DR Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

DR DE PREPROTEIN TRANSLOCASE SECA SUBUNIT.

GN SECA OR TP0379.

OS Treponema pallidum.

OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.

RN [1] SEQUENCE FROM N.A.

RX STRAIN-NICHOLS; 70.

RA MEDLINE; 9833270.

RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 DODSON R., GWYNN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
 SODEGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
 RA McDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJI C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WAYTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.,
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete."

RT Science 281:375-388(1998).

CC -----

CC -I- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SEC60
 SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF
 ATP TO THE TRANSFER OF PRO-SECRETORY PERPLASMIC AND OTHER
 MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).

CC -----

CC -I- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
 WHICH COMPRISE SEC60, SEC61, SEC62, SEC63, SEC64, SEC65 AND SECY
 (BY SIMILARITY).

CC -----

CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF PLASMA MEMBRANE
 (BY SIMILARITY).

CC -----

CC -I- SIMILARITY: BELONGS TO THE SEC60 FAMILY.

CC -----

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 or send an email to license@isb-sib.ch).

CC -----

CC DR EMBL; AE001217; AAC65365.1; --.

DR TIGR; TP0379; --.

DR PFAM; PF01043; SEC60_protein; 1.

DR Protein transport; ATP-binding; Membrane; Translocation; Transport.

KW NP_BIND 103 110 ATP (POTENTIAL)

FT SEQUENCE 916 AA; 103779 MW; 84D5AFAC CRC32;

SQ -----

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CC -----

CC DR EMBL; X80194; CAA55480.1; --.

DR PIR; S47023; S47023.

DR PROSITE; PS00446; RNA_POL-D_30KD; 1.

DR RNA-directed RNA Polymerase; Transcription,
 Transferase; DNA-directed RNA Polymerase; Transcription,
 Sequence 264 AA; 29812 MW; C55B491B CRC32;

DR -----

DR Query Match 30.7%; Score 62; DB 1; Length 264;
 Best Local Similarity 47.4%; Pred. No. 6.40e-01; O;

DR Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

DR DE PREPROTEIN TRANSLOCASE SECA SUBUNIT.

GN SECA OR TP0379.

OS Treponema pallidum.

OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.

RN [1] SEQUENCE FROM N.A.

RX STRAIN-NICHOLS; 70.

RA MEDLINE; 9833270.

RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 DODSON R., GWYNN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
 SODEGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
 RA McDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJI C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WAYTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.,
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete."

RT Science 281:375-388(1998).

CC -----

CC -I- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SEC60
 SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF
 ATP TO THE TRANSFER OF PRO-SECRETORY PERPLASMIC AND OTHER
 MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).

CC -----

CC -I- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
 WHICH COMPRISE SEC60, SEC61, SEC62, SEC63, SEC64, SEC65 AND SECY
 (BY SIMILARITY).

CC -----

CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF PLASMA MEMBRANE
 (BY SIMILARITY).

CC -----

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 or send an email to license@isb-sib.ch).

CC -----

CC DR EMBL; AE001217; AAC65365.1; --.

DR TIGR; TP0379; --.

DR PFAM; PF01043; SEC60_protein; 1.

DR Protein transport; ATP-binding; Membrane; Translocation; Transport.

KW NP_BIND 103 110 ATP (POTENTIAL)

FT SEQUENCE 916 AA; 103779 MW; 84D5AFAC CRC32;

SQ -----

Query Match Score 62; DB 1; Length 916;
 Best Local Similarity 25.9%; Pred. No. 6.40e-01; Mismatches 11; Indels 0; Gaps 0;
 Matches 7; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Db 433 VVYLSEEKWSAIDKEIKRHTSGPV 459
 Qy 2 vphigorekrasvcpgqkyihpqxnsi 28

RESULT 10
 ID CMG3_BACSU STANDARD; PRT; 98 AA.
 AC P25555;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE COMG OPERON PROTEIN 3 PRECURSOR.
 GN COMG OR COMG3
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/staphylococcus group; Bacillus.
 RN [1] RP SEQUENCE FROM N.A.
 RN RP SEQUENCE FROM N.A.
 RN RP SEQUENCE FROM N.A.
 RN MEDLINE; 9008973.
 RA ALBANO M., BREITLING R., DUBNAU D.A.;
 RT "Nucleotide sequence and genetic organization of the Bacillus
 subtilis comg operon.";
 RL J. Bacteriol. 171:5386-5404(1989).
 [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RA KOBAYASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S.,
 RA SATO T., TAKEUCHI M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDJB databases.
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE; 9010868.
 RA BREITLING R., DUBNAU D.;
 RT "A membrane protein with similarity to N-methylphenylalanine pilins
 is essential for DNA binding by competent Bacillus subtilis";
 RL J. Bacteriol. 172:1499-1508(1990).
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 or send an email to license@isb-sib.ch).

CC DR EMBL; M19019; AAA26395; 1;
 DR PIR; B43663; B43663.
 DR Nodulation.
 CC SQ SEQUENCE 148 AA; 15791 MW; 046FAFEC CRC32;

Query Match Score 60; DB 1; Length 148;
 Best Local Similarity 50.0%; Pred. No. 1.66e-00; Mismatches 6; Indels 2; Gaps 0;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 99 REMTCOPNRICH 110
 Qy 11 rdsvepgqkyih 22

RESULT 12
 ID YB18_SCHPO STANDARD; PRT; 140 AA.
 AC P87173;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 35, Last sequence update)
 DE HYPOTHETICAL
 GN SPBC26_08C.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Schizosaccharomyces pombe (Fission Yeast).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA HILBERT H., DUISTERHOFT A., WOOD V., RAJANDREAM M.A., BARRELL B.G.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDJB databases.
 CC - SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC - SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY. STRONG TO
 CC YEAST YJL124C.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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AC P12780;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE NODULATION PROTEIN NOLJ (HOST-INDUCIBLE PROTEIN B).
 GN NOLJ.
 OS Rhizobium fredii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 RN RP SEQUENCE FROM N.A.
 RN MEDLINE; 8808684.
 RA SADOWSKY M.J., OLSON E.R., FOSTER V.E., KOSSIAK R.M., VERMA D.P.S.;
 RT "Two host-inducible genes of Rhizobium fredii and characterization of
 the inducing compound.";
 RL J. Bacteriol. 170:171-178(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA BOURDIE-MILLIS K.L., KOSSIAK R.M., TULLY R.E., PUERPKE S.G.,
 RA LORKE S.M., SADOWSKY M.J.;
 RT "Induction of the Rhizobium fredii nod box-independent nodulation gene
 nolj requires a functional nodB1 gene.";
 RL Mol. Plant Microbe Interact. 7:305-308 (1994).
 CC - FUNCTION: INVOLVED IN EFFICIENCY OF SOYBEAN NODULATION AND IN
 MODULATION DELAY.
 - INDUCTION: BY PLANT 4',7-DIHYDROXY-ISOFLAVONE OR DERIVATIVES.

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 or send an email to license@isb-sib.ch).

CC DR EMBL; L26967; AAA26344; 1; -.
 DR PIR; B43663; B43663.
 DR Nodulation.
 CC SQ SEQUENCE 148 AA; 15791 MW; 046FAFEC CRC32;

Query Match Score 60; DB 1; Length 148;
 Best Local Similarity 50.0%; Pred. No. 1.66e-00; Mismatches 6; Indels 2; Gaps 0;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 99 REMTCOPNRICH 110
 Qy 11 rdsvepgqkyih 22

RESULT 12
 ID YB18_SCHPO STANDARD; PRT; 140 AA.
 AC P87173;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 35, Last sequence update)
 DE HYPOTHETICAL
 GN SPBC26_08C.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Schizosaccharomyces pombe (Fission Yeast).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA HILBERT H., DUISTERHOFT A., WOOD V., RAJANDREAM M.A., BARRELL B.G.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDJB databases.
 CC - SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC - SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY. STRONG TO
 CC YEAST YJL124C.
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RESULT 11
 ID NOJU_RHIFR STANDARD; PRT; 148 AA.

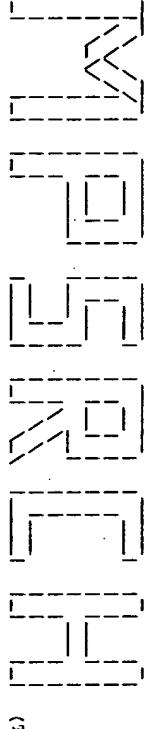
Db 408 HYGHRKTYSECDPCTY 424
 ID G6P1_CLAMT STANDARD; PRT; 568 AA.
 AC P54237;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1995 (Rel. 34, Last annotation update)
 DE GLUCOSE 6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI) (EC 5.3.1.9)
 DE (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI).
 GN PGCL.
 OS Clarkia mildrediae.
 OC Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicots; ledans; Clarkia.
 RN [1]
 RP STRAIN=POPULATION WEEDEN 165A;
 RC RA GOTTLIEB L.D.; FORD V.S.;
 RT "Phylogenetic relationships among the sections of Clarkia (Onagraceae)
 inferred from the nucleotide sequences of PgIC.";
 RL Syst. Bot. 21:1-16(1996).
 CC -- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE = FRUCTOSE 6-PHOSPHATE.
 CC -- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
 CC -- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -- SIMILARITY: BELONGS TO THE GPI FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC
 DR EMBL; XAP9389; CAAC1569_1; --;
 DR PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
 DR PFAM; PF00342; PG1; 1.
 KW Gluconeogenesis; Glycolysis; Isomerase; Multigene family.
 SQ SEQUENCE 568 AA; 62664 MW; 703D6218 CRC32;

Query Match, 29.2%; Score 59; DB 1; Length 568;
 Best Local Similarity 41.7%; Pred. No. 2.65e+00;
 Matches 10; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Db 95 VLMVALRAPRDSATCSDGRKNNVPPD 118
 Qy 1 | :| :| || :|| :|| :|:
 2 vphgdrkrdsvcpq9kyihp 24

Search completed: Tue Apr 18 11:07:36 2000
 Job time : 31 secs.

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(TM)

MSRCH_PP Protein - Protein database search, using Smith-Waterman algorithm
 Run on: Tue Apr 18 11:07:54 2000; MasPar time 66.86 Seconds
 Tabular output not generated.

Title: >PEP1..PEP
 Description: (1-28) from new.pep
 perfect Score: 202
 Sequence: 1 lvphlgdrekrdsvcpqky1hpqns1 28

Scoring table: PAM 150
 Gap 15

Searched: 225878 seqs, 69334122 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:
 sptrembl12

1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phage 10:sp_plant 11:sp_rabbit 12:sp_uncharacterized
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 28.745; Variance 34.322; scale 0.837

*pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	167	82.7	189	6	095185	1
2	149	73.8	471	6	019131	TUMOUR NECROSIS FACTOR-
3	145	71.8	189	6	097530	TUMOR NECROSIS FACTOR
4	74	36.6	213	2	032029	YRT PROTEIN
5	69	34.2	132	11	035324	BMS/FLL ACTIVATED TRA
6	68	33.7	483	3	094206	OXIDOREDUCTASE
7	66	32.7	467	5	05993	PICHIT-3
8	65	32.2	687	5	023729	THROMBOSPDIN RELATED
9	65	32.2	1376	5	026637	5 ALPHA FIBRILLAR COLL
10	65	32.2	1724	5	025425	P-GLYCOPROTEIN
11	63	31.2	505	10	065727	SQUALENE EPOXIDASE HOM
12	63	31.2	518	10	065726	SQUALENE EPOXIDASE HOM
13	63	31.2	563	14	082794	L-PROTEIN
14	62	30.7	307	10	09XII1	F7H1.9 PROTEIN
15	62	30.7	414	5	025308	SQUALENE SYNTHASE
16	62	30.7	563	2	052208	ACTIVATOR
17	62	30.7	699	1	09YFR1	699AA LONG HYPOTHETICA
18	62	30.7	774	3	042918	PUTATIVE ALPHA-AMYLASE
19	62	30.7	1187	2	059278	ENDOXYLAMINASE (EC 3.2.1.304+00
20	30.7	2664	5	026033	VARIANT-SPECIFIC SURFA	

ALIGNMENTS

ID Q95185;	RESULT 1	PRELIMINARY;	PRT; 189 AA.
AC Q95185;	ID	Q95185;	PRT; 189 AA.
DT 01-FEB-1997 (TREMBLER, 02, Created)	DT	01-FEB-1997 (TREMBLER, 06, Last sequence update)	
DT 01-JUN-1999 (TREMBLER, 12, Last annotation update)	DT	01-JUN-1999 (TREMBLER, 12, Last annotation update)	
DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).	DE	TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).	
GN TNFR-1.	GN	TNFR-1.	
OS Felis silvestris catus (Cat).	OS	Felis silvestris catus (Cat).	
OC Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	OC	Eutheria; Carnivora; Fissipedia; Felidae; Felis.	
RN [1].	RN	[1].	
SEQUENCE FROM N.A.			
RA DUTHIE S., NASIR L., ECKERSON P.D.;	RA	DUTHIE S., NASIR L., ECKERSON P.D.;	
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	
EMBU: 072344; AAB95089 1;	EMBU:	072344; AAB95089 1;	
DR HSSP; P19438; TEXT.	DR	HSSP; P19438; TEXT.	
DR PROSITE; PS00652; TNFR.NGFR.1; 3.	DR	PROSITE; PS00652; TNFR.NGFR.1; 3.	
DR PFAM; PF00020; TNFR.C6; 3;	DR	PFAM; PF00020; TNFR.C6; 3;	
FT NON-TER 189 AA; 21420 MM; 667732d2 CRC32;	FT	NON-TER 189 AA; 21420 MM; 667732d2 CRC32;	
SQ SEQUENCE	SQ	SEQUENCE	
Query Match 82.7%; Score 167; DB 6; Length 189;			
Best Local Similarity 82.1%; Pred. No. 4.88e-29; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			
Db 30 LVPHLGDRKRDVCPQKGKY1HPQNS1 57	Db	30 LVPHLGDRKRDVCPQKGKY1HPQNS1 57	
Qy 1 lvphlgdrekrdsvcpqky1hpqns1 28	Qy	1 lvphlgdrekrdsvcpqky1hpqns1 28	
RESULT 2			
PRELIMINARY; PRT; 471 AA.			
AC 019131; DT 01-JAN-1998 (TREMBLER, 05, Created)	AC	019131; DT 01-JAN-1998 (TREMBLER, 05, Last sequence update)	
DT 01-NOV-1999 (TREMBLER, 12, Last annotation update)	DT	01-NOV-1999 (TREMBLER, 12, Last annotation update)	
DE TUMOR NECROSIS FACTOR-RECEPTOR I.	DE	TUMOR NECROSIS FACTOR-RECEPTOR I.	
GN TNFR-1.	GN	TNFR-1.	
OS Bos taurus (Bovine).	OS	Bos taurus (Bovine).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
OC Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;	OC	Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;	
RN [1].	RN	[1].	

RP SEQUENCE FROM N.A.
 RC TISSUE=AORTA;
 RA LEE E.-K., TALIVOR M.J., KEHRLI M.E.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U90937; AAB65143.1; -.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS0052; TNFR_NGFR_1; 3.
 DR PFAM; PF0053; death; 1.
 DR PFF00020; TNFR_C6; 3.
 SQ SEQUENCE 471 AA; 51367 MW; 1D60FF4A CRC32;

Query Match 73.8%; Score 149; DB 6; Length 471;
 Best Local Similarity 71.4%; Pred. No. 1.26e-23;
 Matches 20; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 lvphgdrrekrdsvcpqkyihpxnsi 28

RESULT 3 PRELIMINARY; PRT; 189 AA.
 ID 097530
 AC 097530
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eukaryota; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA DUTHIE S., NASIR L., ARGYLE D.J., ECKERSALL P.D.;
 RT "Canine tumor necrosis factor receptor, partial cds.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF013955; AAD01516.1; -.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 KW Receptor.
 FT NON_TER 189
 SQ SEQUENCE 189 AA; 21324 MW; 24A93EBF CRC32;

Query Match 71.8%; Score 145; DB 6; Length 189;
 Best Local Similarity 67.9%; Pred. No. 1.93e-22;
 Matches 19; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 30 IVPHPHRNVRKRAILCPQGKVYHPODDSI 57
 QY 1 lvphgdrrekrdsvcpqkyihpxnsi 28

RESULT 4 PRELIMINARY; PRT; 213 AA.
 ID 032029
 AC 032029
 DT 01-JUN-1998 (TREMBLrel. 05, created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DE YVRT PROTEIN.
 GN YVRT
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 SQ SEQUENCE 4 AA; 189 MW; 1D60FF4A CRC32;

Query Match 34.2%; Score 69; DB 11; Length 132;
 Best Local Similarity 31.4%; Pred. No. 1.26e-23;
 Matches 20; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 lvphgdrrekrdsvcpqkyihpxnsi 28

RESULT 5 PRELIMINARY; PRT; 132 AA.
 ID 035324
 AC 035324
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE EWS/FEL1 ACTIVATED TRANSCRIPT 2.
 GN EAT-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinata; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97152556.
 RA THOMSON A.D., BRAIN B.S., ARVAND A., STEWART S.D., MAY W.A., CHEN E.,
 RA KORENBERG J., DENNY C.T.,
 RT "EAT-2 is a novel SH2 domain containing Protein that is up regulated
 by Ewing's sarcoma EWS/FEL1 fusion gene.";
 RL Oncogene 13:2649-2658(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA THOMSON A.D., BRAIN B.S., ARVAND A., STEWART S.D., MAY W.A., CHEN E.,
 RA KORENBERG J., DENNY C.T.,
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF020263; AAB70923.1; -.
 DR HSSP; P1931; ISHD.
 DR PFAM; PF00017; SH2; 1.
 SQ SEQUENCE 132 AA; 15258 MW; 3126FD44 CRC32;

Query Match 34.2%; Score 69; DB 11; Length 132;

RESULT 10 PRELIMINARY; PRT; 1724 AA.

ID Q25425; PRELIMINARY; PRT; 1724 AA.

AC 025425; PRELIMINARY; PRT; 1724 AA.

DT 01-NOV-1996 (TREMBrel. 01, Created)

DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBrel. 12, Last annotation update)

DE P-GLYCOPROTEIN.

OS leishmania tarentolae (Sauroleishmania tarentolae); Leishmania.

OC Bokaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

RP SEQUENCE FROM N.A.

RC STRAIN=TAR1;

RX MEDLINE: 95198776.

RA LEGARE D., HETTMAN E., OUSLIETTE M.;

RT "The P-glycoprotein-related gene family in leishmania.";

RL Mol. Biochem. Parasitol. 68:81-91(1994).

DR EMBL: U23455; AAC:65541.1; -.

DR HSPP: P13669; INDB: 188967 MW; C9F31C24 CRC32;

DR PFAM: PF00064; ABC_membrane; 2.

DR PFAM: PF00005; ABC_tran; 2.

SQ SEQUENCE 1724 AA; 188967 MW; C9F31C24 CRC32;

Query Match 32.2%; Score 65; DB 5; Length 1724;

Best Local Similarity 40.2%; Pred. No. 3.04e-01; Mismatches 6; Conservative 6; Indels 3; Gaps 0;

Matches 6; Mismatches 3; Indels 0; Gaps 0;

Db .913 LDAAHGVRRVMRBCIC 927

OY 1 lvphlgdrekrdsvc 15

RESULT 11 PRELIMINARY; PRT; 506 AA.

ID 065727; PRELIMINARY; PRT; 506 AA.

AC 065727; PRELIMINARY; PRT; 506 AA.

DT 01-AUG-1998 (TREMBrel. 07, Created)

DT 01-AUG-1998 (TREMBrel. 07, Last sequence update)

DT 01-NOV-1999 (TREMBrel. 12, Last annotation update)

DE SQUALENE EPoxidase homologue (EC 1.14.99.7).

GN SQP1.2.

OS Brassica napus (Rape).

OC Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicidae; Brassicaceae.

RC STRAIN=CV; WESTAR; TISSUE=SHOOTS;

RX SEQUENCE FROM N.A.

RA SCHAFER U.A., REED D.W., HUNTER D.G., YAO K., WENINGER A.M., TSANG E.W., REANEY M.J.T., MACKELZIE S.L., COVELLO P.S.;

RL Submitted (MAY 1998) to the EMBL/GenBank/DDJB databases.

DR EMBL: AJ005928; CAA:06770.1; -.

MENDL: 28850; Brana:3393; 29850.

KW Oxidoreductase; SEQUENCE 518 AA; 5740 MW; 5F2B687E CRC32;

DR PFAM: PF00064; ABC_membrane; 2.

DR PFAM: PF00005; ABC_tran; 2.

SQ SEQUENCE 518 AA; 5740 MW; 5F2B687E CRC32;

Query Match 31.2%; Score 63; DB 10; Length 518;

Best Local Similarity 30.0%; Pred. No. 8.05e-01; Mismatches 9; Conservative 6; Indels 0; Gaps 0;

Matches 6; Mismatches 5; Indels 0; Gaps 0;

Db 75 HVIERDMDPYPVMMGSEMQP 94

OY 4 hlgdrekrdsvcpqgkyihp 23

RESULT 13 PRELIMINARY; PRT; 563 AA.

ID 082794; PRELIMINARY; PRT; 563 AA.

AC 082794; PRELIMINARY; PRT; 563 AA.

DT 01-NOV-1995 (TREMBrel. 01, Created)

DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBrel. 12, Last annotation update)

DE L PROTEIN.

GN MAGI9NE.

OS Influenza A virus.

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A/FFV/DUTCH/27 (HTNT), DUTCH;

RA MUNK K., PRITZER E., KRETSCHMAR E., GUTTE B., GARTEN W., KLENK H.,

RL Glycobiology 0-0-0(1992);

DR EMBL: Z1261; CAA:78203.1; -.

DR PFAM: PF00509; Hemagglutinin; 1.

DR PRINTS; PRO0329; Hemagglutinin; 1.

DR PRINTS; PRO0330; Hemagglutinin; 2.

SQ SEQUENCE 563 AA; 62883 MW; 6D36PAC1 CRC32;

Query Match 31.2%; Score 63; DB 14; Length 563;

Best Local Similarity 33.3%; Pred. No. 8.05e-01; Mismatches 6; Conservative 6; Indels 0; Gaps 0;

Matches 6; Mismatches 6; Indels 0; Gaps 0;

Db 97 ERRERNIDVCPCKFVNGE 114

OY 7 drekrdsvcpqgkyihp 24

RESULT 14 PRELIMINARY; PRT; 307 AA.

ID Q9XII1; PRELIMINARY; PRT; 307 AA.

AC Q9XII1; PRELIMINARY; PRT; 307 AA.

DT 01-NOV-1999 (TREMBrel. 12, Created)

DT 01-NOV-1999 (TREMBrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBrel. 12, Last annotation update)

DE F7H1.9 PROBIN.

GN F7H1.9.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

RC STRAIN=CV; WESTAR; TISSUE=SHOOTS;

RX SEQUENCE FROM N.A.

RA SCHAFER U.A., REED D.W., HUNTER D.G., YAO K., WENINGER A.M., TSANG E.W., REANEY M.J.T., MACKELZIE S.L., COVELLO P.S.;

RL Submitted (MAY 1998) to the EMBL/GenBank/DDJB databases.

DR EMBL: AJ005928; CAA:06770.1; -.

MENDL: 28850; Brana:3393; 29850.

KW Oxidoreductase; SEQUENCE 518 AA; 5740 MW; 5F2B687E CRC32;

DR PFAM: PF00064; ABC_membrane; 2.

DR PFAM: PF00005; ABC_tran; 2.

SQ SEQUENCE 518 AA; 5740 MW; 5F2B687E CRC32;

Query Match 31.2%; Score 63; DB 10; Length 506;

Best Local Similarity 30.0%; Pred. No. 8.05e-01; Mismatches 6; Conservative 6; Indels 0; Gaps 0;

Matches 6; Mismatches 5; Indels 0; Gaps 0;

Db .74 HVIERDMDPYPVMMGSEMQP 93

OY 4 hlgdrekrdsvcpqgkyihp 23

RESULT 12 PRELIMINARY; PRT; 518 AA.

ID 065726 PRELIMINARY; PRT; 518 AA.

AC 065726; PRELIMINARY; PRT; 518 AA.

DT 01-AUG-1998 (TREMBrel. 07, Created)

RN	OC arabidopsis.
RP	[1] SEQUENCE FROM N.A.
RC	STRAIN=CV. COLUMBIA;
RA	LIN X., KAUL S., SHEA T.P., FUJI C.Y., SHEN M., VANAKEN S.E.,
RA	CARRERA A.J., CHEASY T.H., BUELL C.R., TOWN C.D., NIERNAN W.C.,
RA	FRASER C.M., VENIER J.C.;
RT	"Arabidopsis thaliana chromosome II BAC F7H1 genomic sequence.";
RL	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AAC001134; AAC24950.1; -.
SQ	SEQUENCE 307 AA; 33640 MW; 079B17E6 CRC32;
	Query Match 30.7%; Score 62; DB 10; Length 307;
	Best Local Similarity 30.7%; Pred. No. 1.30e+00;
Matches	10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
Db	253 LIPHRATRGKRPQDPPGK 272
QY	: :
	1 lvphlgdrekrdsv-cqpgk 19
RESULT 15	
ID 025308	PRELIMINARY;
AC Q25308;	PRT; 414 AA.
DT 01-NOV-1996 (TREMBREL. 01, Created)	
DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)	
DT 01-NOV-1998 (TREMBREL. 08, Last annotation update)	
DE SQUALENE SYNTHASE.	
OS Leishmania major.	
OC Eukaryota; Euglenozoa; Kinetoplastida; trypanosomatidae; Leishmania.	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=FRIEDLIN VI;	
RA GOTTM P.C., GARRITY L., BEVERLEY S.M.;	
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.	
DR EMBL; U30455; AAC17923.1; -.	
DR PRAM; PF00594; SOS_PSY; 1.	
DR SEQUENCE 414 AA; 4684. MW; FB8AA048 CRC32;	
Query Match 30.7%; Score 62; DB 5; Length 414;	
Best Local Similarity 40.0%; Pred. No. 1.30e+00;	
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;	
Db . 48 VVAQLADQQLRDAIC 62	
QY . : :	
1 lvphlgdrekrdsv 15	

:32 2000

PEPL. PEP. rag

AC R10984;	CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
DT 13-MAY-1991 (first entry)	SQ Sequence 154 AA;
DE Partial sequence 30KD TNF inhibitor.	Query Match 100.0%: Score 202; DB 1; Length 154;
KW tumour necrosis factor; inhibitor.	Best Local Similarity 96.4%; Pred. No. 1.00e-16;
OS Homo sapiens.	Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Key	FT Location/Qualifiers
region	1..52
FT /label= exon I	PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
FT /label= exon II	PR 18-OCT-1990; GB-022648.
FT /label= exon III	DR 30 LYPHLGDRERKRDSCVCPQKYIHPQNSI 57
FT /ncte= "incomplete"	OY 1 lyphlgdrerkrdsbcvcpqkyihpqnsi 28
PA (SYNE-) SENERGEN INC.	
PN WPI; 91-073847/1L.	
DR N-PSDB; Q10878.	
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha	
PT and -beta, useful as therapeutic agent.	
PT Disclosure: Fig 13; 142PP; English.	
PS The sequence comprises 48 residues of the 30 KD TNF inhibiting	
CC glycoprotein, in three exons. The clone from which the sequence	
CC was obtid. was isolated from a human genomic library. The whole	
CC gene can be inserted into expression vectors for prepn. of TNF	
CC inhibitor for use in the treatment of inflammatory and degenerative	
CC diseases.	
CC See also R10986 and R11001.	
SQ Sequence 102 AA;	
RESULT 3	
ID R24082 standard; Protein; 154 AA.	
AC R24082;	Query Match 100.0%; Score 202; DB 1; Length 102;
DT 05-Nov-1992 (first entry)	Best Local Similarity 96.4%; Pred. No. 1.00e-16;
DE Truncated TNF-55kD receptor.	Mismatches 0; Indels 0; Gaps 0;
KW tumour necrosis factor alpha; extracellular binding domain; AIDS;	
KW treatment; pulmonary diseases; septic shock; HIV infection;	
KW malaria; viral meningitis; graft versus host disease;	
KW autoimmune disease; rheumatoid arthritis.	
OS Homo sapiens.	
PN WO9207076-A.	
PT 30-APR-1992.	
PR 18-OCT-1991; Q01826.	
CC (CHAR-) CHARING CROSS SUNLEY RES CENT.	
CC PA (CHAR-) CHARING CROSS SUNLEY RES CENT.	
CC PI Brennan FM, Feldmann M, Gray PW, Turner MJC;	
CC DR WPI; 92-167156/20.	
PT New polypeptide capable of binding human TNF alpha - comprises	
PT first three cysteine-rich subdomains of TNF alpha receptor for	
PT treating autoimmune disease, septic shock, HIV etc.	
PS Example 1; Fig 10; 43PP; English.	
CC This sequence is a truncated TNF-alpha receptor derivative	
CC as encoded in detail. This was produced as described in	
CC CC 024444. This derivative lacks the third cysteine rich subdomain:	
CC It could be used to regulate TNF-alpha mediated responses by binding	
CC and sequestering human TNF-alpha e.g. in the treatment of pulmonary	
CC diseases, septic shock, HIV infection, malaria, viral meningitis, id	
CC graft versus host disease and autoimmune diseases, esp. rheumatoid	
CC arthritis.	
CC See also Q24440-51; R24000, R24080-84, R27585, Q29236-8	
SQ Sequence 159 AA;	
RESULT 3	Query Match 100.0%; Score 202; DB 1; Length 159;
ID R24084 standard; Protein; 168 AA.	Best Local Similarity 96.4%; Pred. No. 1.00e-16;
AC R24084;	Mismatches 1; Indels 0; Gaps 0;
DT 05-Nov-1992 (first entry)	
DE Truncated TNF-alpha 55kD receptor.	
DE tumour necrosis factor alpha; extracellular binding domain; AIDS;	
DE treatment; pulmonary diseases; septic shock; HIV infection;	
DE malaria; viral meningitis; graft versus host disease;	
DE autoimmune disease; rheumatoid arthritis.	
OS Homo sapiens.	
PN WO9207076-A.	
PT 30-APR-1992.	
PR 18-OCT-1990; GB-022648.	
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.	
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;	
DR WPI; 92-167156/20.	
PT New polypeptide capable of binding human TNF alpha - comprises	
PT first three cysteine-rich subdomains of TNF alpha receptor for	
PT treating autoimmune disease, septic shock, HIV etc.	
PS Example 1; Fig 9; 43PP; English.	
CC This sequence is a truncated TNF-alpha receptor derivative	
CC as encoded in detail. This was produced as described in	
CC Q24443. This derivative lacks the third cysteine rich subdomain.	
CC It could be used to regulate TNF-alpha mediated responses by binding	
CC and sequestering human TNF-alpha e.g. in the treatment of pulmonary	
CC diseases, septic shock, HIV infection, malaria, viral meningitis,	
CC graft versus host disease and autoimmune diseases, esp. rheumatoid	
CC arthritis.	
CC See also Q24440-51; R24000, R24080-84, R27585, Q29236-8	
SQ Sequence 159 AA;	
RESULT 5	Query Match 100.0%; Score 202; DB 1; Length 159;
ID R24084 standard; Protein; 168 AA.	Best Local Similarity 96.4%; Pred. No. 1.00e-16;
AC R24084;	Mismatches 1; Indels 0; Gaps 0;
DT 05-Nov-1992 (first entry)	
DE Truncated TNF-alpha 55kD receptor.	
DE tumour necrosis factor alpha; extracellular binding domain; AIDS;	
DE treatment; pulmonary diseases; septic shock; HIV infection;	
DE malaria; viral meningitis; graft versus host disease;	
DE autoimmune disease; rheumatoid arthritis.	
OS Homo sapiens.	
PN WO9207076-A.	
PT 30-APR-1992.	
PR 18-OCT-1990; GB-022648.	
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.	
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;	
DR WPI; 92-167156/20.	
PT New polypeptide capable of binding human TNF alpha - comprises	

PT first three cysteine-rich subdomains of TNF alpha receptor for
 PT treating autoimmune disease; septic shock; HIV etc.
 PS Example 1; FIG 11; 43PP; English.
 CC This sequence is a truncated TNF-alpha receptor derivative, as
 encoded in peptideIV. This was produced as described in Q2445.
 CC This derivative lacks the membrane proximal 4th subdomain, yet
 retains the ability to bind TNF-alpha with high affinity
 (10^{power8} - 10^{power9} Mpower⁻¹) The deriv. can be used in the
 regulation of TNF-alpha mediated responses by binding and
 sequestering human TNF-alpha e.g. in the treatment of pulmonary
 diseases, septic shock, HIV infection, malaria, viral meningitis,
 graft versus host disease and autoimmune diseases, esp. rheumatoid
 arthritis. The deriv. is given at 10-100ug/dose.
 CC See also Q2444-51, R24000, R24080-84, R27585, Q29236-8
 SQ Sequence 168 AA;

Query Match 100.0%; Score 202; DB 1; Length 168;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16; Mismatches 27; Conservative 0; Indels 1; Gaps 0; OS
 Matches 27; Mismatches 1; Indels 0; Gaps 0; PT
 Db 30 LVPHIGDRKRDSDVCPQGYIHPONSI 57
 QY 1 lvphigdrkrdsvcpqgyihpnsi 28

RESULT 6
 ID R24080 standard; protein; 199 AA.
 AC R24080; 30
 DT 05-NOV-1992 (first entry)
 DE Truncated TNF-alpha 55kd receptor.
 KW tumour necrosis factor alpha; extracellular binding domain;
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
 KW malaria; viral meningitis; graft versus host disease;
 KW autoimmune disease; rheumatoid arthritis.
 OS Homo sapiens.
 PN WO920706-A.
 PD 30-APR-1992.
 PR 18-OCT-1991; G01826.
 PR 18-OCT-1990; GB-022648.

PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
 PI Brennan RM, Feldmann M, Gray PW, Turner MJC;
 DR WRI; 92-167156/20.
 DR N-PSDB; 02441.
 PT New polypeptide capable of binding human TNF alpha - comprises
 PT first three cysteine-rich subdomains of TNF alpha receptor for
 PT treating autoimmune disease; septic shock, HIV etc.
 PS Example; FIG 7; 43PP; English.
 CC This sequence is a truncated TNF-alpha receptor derivative, as encoded
 in peptideIV. This was produced as described in Q24440.
 CC This derivative lacks the 81 carboxyl terminal residues of the
 cytoplasmic domain. The derivative could be used in the
 regulation of TNF-alpha mediated responses by binding and
 sequestering human TNF-alpha e.g. in the treatment of pulmonary
 diseases, septic shock, HIV infection, malaria, viral meningitis,
 graft versus host disease and autoimmune diseases, esp. rheumatoid
 arthritis.
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
 SQ Sequence 199 AA;

Query Match 100.0%; Score 202; DB 1; Length 211;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16; Mismatches 27; Conservative 0; Indels 1; Gaps 0; OS
 Matches 27; Mismatches 1; Indels 0; Gaps 0; PT
 Db 30 LVPHIGDRKRDSDVCPQGYIHPONSI 57
 QY 1 lvphigdrkrdsvcpqgyihpnsi 28

RESULT 8
 ID R70108 standard; protein; 309 AA.
 AC R70108; 30
 DT 10-NOV-1995 (first entry)
 DE TNF-R-GBP fusion protein.
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
 KW red blood cell; cytokine receptor; glycophorin binding peptide 130;
 KW GBP 130; GBP130; glycophorin binding peptide homologue; glycophorin A;
 KW tumour necrosis factor receptor; TNF-R.
 OS Chimeric Homo sapiens.
 OS Chimeric Plasmodium falciparum.
 FH Key Location/Qualifiers
 FT misc_difference 230_269
 FT /label=repeat_region
 FT /note= "can be repeated n times, where n is a real
 number"
 FN WO9506737-A.
 PD 09-MAR-1995.
 PF 01-SEP-1994; G01900.
 PR 03-SEP-1993; GB-018350.
 PR 23-AUG-1994; GB-017021.
 PA (PREN/)- PREENDERGAST K F.
 PI Prendergast KR;
 DR WPI-95-111452/15.
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a
 PT malaria parasite Peptide capable of binding a red blood cell and
 PT a receptor peptide.
 PS Example A; Page 54-55; 93PP; English.
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite.

CC Clone pTNF-BP15 was used to construct pTNF-BP, for transfection of
CC e.g. COS7 cells. The expressed proteins are useful
CC prophylactically and therapeutically to control disorders which
CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC respiratory distress syndrome etc., or side effects of treatment with
CC TNG-alpha). They can also be used as diagnostic reagents for
CC assaying TNF and in study of TNF-receptor interactions.
CC See also 006282-006285.

SQ Sequence 371 AA;

Query Match Best Local Similarity 100.0%; Score 202; DB 1; Length 371;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 30 LVPHIGDREKRDSVCPQGYVHPPONNSI 57

Oy 1 lvpfhigdrekrdsvcpqgyvhpponsi 28

RESULT 12

ID W89227 standard; Protein: 397 AA.

AC W89227; 04-MAR-1999 (first entry)

DT DE Tumour necrosis factor bp/osteoprotegerin construct TNFBP/196.

KW KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;

INflammation; apoptosis; Homo sapiens.

OS OS Synthetic.

PR PN W09849305-A1.

PD PD 05-NOV-1998.

PF PF 29-APR-1998; US-850188.

PA PA (AMGE-) AMGEN INC.

PI PI Boyle WJ, Wooden S;

DR DR WPI; 99-034661/03.

PT PT New chimeric osteoprotegerin polypeptides - contain the

osteoprotegerin dimerisation domain and a heterologous sequence,

PS PS useful to treat TNF and TNFR-mediated disorders

Example 1, Fig 4; 92pp; English.

The present invention describes a chimeric polypeptide (Al), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous

amino acid sequence. Also described are: (1) a multimer polypeptide

comprising covalently associated Al monomers; (2) an isolated nucleic

acid encoding Al; (3) an expression vector comprising the nucleic acid

sequence; and (4) a host cell transformed or transfected with the

expression vector so that the nucleic acid is expressible. The products

from the present invention are useful to treat a variety of disorders

including those related to receptor binding. Compositions comprising

tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras

are used to treat TNF and TNFR-mediated disorders such as inflammation,

autoimmune diseases and disorders related to excessive apoptosis. The

chimeras are also useful for detecting molecules which interact with

ligands. The present sequence represents a TNFBP/OPG construct from

the example of the present invention for creating TNFBP/OPG fusion

proteins.

Sequence 417 AA;

PT PT WPI; 99-034661/03.

PT PT osteoprotegerin dimerisation domain and a heterologous sequence,

useful to treat TNF and TNFR-mediated disorders

Example 1, Fig 4; 92pp; English.

The present invention describes a chimeric polypeptide (Al), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous

amino acid sequence. Also described are: (1) a multimer polypeptide

comprising covalently associated Al monomers; (2) an isolated nucleic

acid encoding Al; (3) an expression vector comprising the nucleic acid

sequence; and (4) a host cell transformed or transfected with the

expression vector so that the nucleic acid is expressible. The products

from the present invention are useful to treat a variety of disorders
including those related to receptor binding. Compositions comprising
tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
are used to treat TNF and TNFR-mediated disorders such as inflammation,
autoimmune diseases and disorders related to excessive apoptosis. The
chimeras are also useful for detecting molecules which interact with
ligands. The present sequence represents a TNFBP/OPG construct from
the example of the present invention for creating TNFBP/OPG fusion
proteins.

Query Match Best Local Similarity 100.0%; Score 202; DB 1; Length 417;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 30 LVPHIGDREKRDSVCPQGYVHPPONNSI 57

Oy 1 lvpfhigdrekrdsvcpqgyvhpponsi 28

RESULT 14

ID W89224 standard; Protein: 420 AA.

AC AC W89224;

DT DT 04-MAR-1999 (first entry)

DE DE Tumour necrosis factor bp/osteoprotegerin construct TNFBP/OPG.

KW KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;

INflammation; apoptosis; Homo sapiens.

OS OS Synthetic.

PR PN W09849305-A1.

PD PD 05-NOV-1998.

PF PF 29-APR-1998; US-850188.

PA PA (AMGE-) AMGEN INC.

PI PI Boyle WJ, Wooden S;

DR DR WPI; 99-034661/03.

PT PT New chimeric osteoprotegerin polypeptides - contain the

osteoprotegerin dimerisation domain and a heterologous sequence,

useful to treat TNF and TNFR-mediated disorders

Example 1, Fig 4; 92pp; English.

The present invention describes a chimeric polypeptide (Al), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous

amino acid sequence. Also described are: (1) a multimer polypeptide

comprising covalently associated Al monomers; (2) an isolated nucleic

acid encoding Al; (3) an expression vector comprising the nucleic acid

sequence; and (4) a host cell transformed or transfected with the

expression vector so that the nucleic acid is expressible. The products

CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/ORG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFBp/ORG construct from
 CC the example of the present invention for creating TNFBp/OPG fusion
 CC proteins.

Sequence 420 AA;

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Query Match 100.0%; Score 202; DB 1; Length 420;
Best Local Similarity 96.4%; Pred. No. 1.00e-16; 0; Mismatches 1; Indels 0; Gaps 0;
Matches 27; Conservative 0; Job time : 28 secs.
Db 30 LVPHLGDREREKRDSDVCPQGKYIHPQNNSI 57
QY 1 lvphlgdrerekrdsavcpqgkyihpqxnsi 28
```

RESULT 15
 ID R51032 standard; Protein; 433 AA.
 AC R51032;
 DT 13-MAY-1994 (first entry)
 DE Mutant p55 tumour necrosis factor receptor.
 KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;
 KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
 KW effector protein.
 OS Homo sapiens.
 PH
 FT Key 1..21
 FT region /label= Leader peptide.
 FT domain 103..205
 FT /label= transmembrane domain.
 PN EP-568935-A.
 PD 10-NOV-1993.
 PF 29-APR-1993; 106981.
 PR 03-MAY-1992; IL-101769.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Brakebusch C, Wallach D;
 DR WPI: 93-353057/45.
 DR N-PDB: 050870.
 PT Modulating activity of tumour necrosis factor receptor - using
 PT peptides, antibodies, etc. which interact with critical regions
 PT of receptor or effector protein, for controlling auto-immune
 PT disease, septic shock, etc.
 PS Claim 4; Figure 1; 17pp; English.
 CC Modification of the tumour necrosis factor receptor by mutation or
 CC deletion modulates signal transduction and/or cleavage effected by
 CC the receptor. This modulation of activity can also be achieved
 CC using effector proteins which interact with the TNF receptor.
 CC Molecules which interact with the TNF receptor or the effector
 CC proteins can be used to treat or prevent diseases associated with
 CC TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
 CC rejection; graft vs. host disease or septic shock. They can also
 CC be used to treat overdoses of exogenous TNF. Specific deletions
 CC include amino acid residues 405-426 (to give this sequence, wild
 CC type protein disclosed in R42197) from which it was discovered
 CC that amino acids 405-414, or part of them, are essential for the
 CC signalling of the human p55 TNF-R for the cytotoxic effect of TNF
 CC whereas amino acids 415-426 are not essential. Also residues
 CC 170-174, 174-179 or both i.e. 170-179 were deleted. This region of
 CC amino acids, or part of, when deleted, abolished shedding of the
 CC soluble extracellular forms of the protein.
 SQ Sequence 433 AA;

OY 1 lvphlgdrerekrdsavcpqgkyihpqxnsi 28

Search completed: Tue Apr 18 11:05:38 2000
 Job time : 28 secs.

Query Match 100.0%; Score 202; DB 1; Length 433;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 27; Conservative 0; Job time : 28 secs.

Db 30 LVPHLGDREREKRDSDVCPQGKYIHPQNNSI 57
 QY 1 lvphlgdrerekrdsavcpqgkyihpqxnsi 28